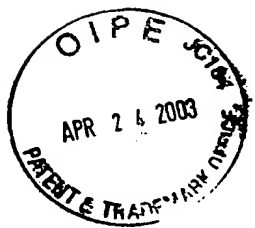


FIG. 3



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```

1                                                    50
RSBEI ..... ***** *....**pl lp***** **ag*****
MSBEI ..... *****v**p** **tplp***r ***h***aa* pg*****
D4cDNA ..... *****ap*c **sl...**p **pa***g* **s*.....
PESBEII .....
POSBE meinfkvlsk pirsfp*f* pkv*sgas*n kic*psqh*t *lkf*sgrs
D2cDNA ..... *****s**ll prp*a*.... ....**l* *****ggk
Consensus ----- -MLCLTSSSS SP-S-APPR- SRS-ADRPSP GIIAGGGNVR

51                                                    100
RSBEI l..**v*... *p*****g** *tn***pa** rk****v*v* ***..*****
MSBEI l..**l**qc ka***gv*** *****ataa*v q*d*****ak g**..*****
D4cDNA ..... *****p*s* prdy*****a* *g*..gd***
PESBEII ..... .....mt d*ks**psv* **f*..nig*
POSBE w..d*s*t*k *rv*kde*mk h*saisa*lt d*s***pl* ***kt*nigl
D2cDNA rlsv*p***f ll**l*****a ***sf*s*** rg**ia**.. tgygs*****
Consensus ---SV-SVP- S-RRSWPRKV KSKFSV-VTA -DNKTMAT-E EDV--DHLPI

101                                                    150
RSBEI *****e* *****n**i** *****c***** *****v
MSBEI *****i* ***** *****gs**e n**s**s*** *****n
D4cDNA *****ag* *****s***** *****s*** *****
PESBEII lnv*ss**p* *****k***** **h**k***e y****q**a* *****f*r*
POSBE ln***t**p* l****h**** *v***m**** y**p****aq *****f*r*
D2cDNA *****l**ae* *****d*trn* *i***** *****s***** *****
Consensus YDLDPKLE-F KDHFYRMKR YLDQKHLIEK HEGGLEEF SK GYLKFGINTE

151                                                    200
RSBEI *g***** ***** *****ak* *****k***** **k*****
MSBEI *dg***** *****e*** *****d***a** *****k***** **k*d**k**
D4cDNA nd***** *****m***** *****g* r*t**n**** *****
PESBEII *dgis***** *****i** *****g*****l h*****q***** **q*pdad*n
POSBE *gci***** *****dev** *****g***** m*****q***** *****pd*ds*
D2cDNA hg*s***** *****e***** *****g***** **a**n**** *****
Consensus --ATVYREWA PAAQEAQLIG DFNNWNGSNH KMEKD-FGVW SIRISHVNGK

201                                                    250
RSBEI ***** *****r**g*a* ***** *****f***** *****
MSBEI ***** *****l*.g*** *****l*** ***** *****
D4cDNA ***** *****hr*d*l* ***** *****f***** *****
PESBEII *****r** *****k*sd*** *****k* *****ptr*a* *****y****
POSBE *v*****r** *****k**n*** *****k* **a**t**a* *****y****
D2cDNA ***** *****r*.h*** **q***** *****t**es** *****l*****
Consensus PAIPHNSKVK FRF-HG-GVW VDRIPAWIRY ATVDASKFGA PYDGVHWDPP

251                                                    300
RSBEI ac***** ***** ***** ***** *****
MSBEI a*****t**** **s**a***** ***** *****k*a***** *****
D4cDNA sg***** **r***** ***** *****r***** *****k*
PESBEII l****q**** *****k**** *****ss **r*ns**** **d*****e
POSBE p****h*y* *****r**** *****ss **r*ns**** **d*****k*
D2cDNA s*****n** *****v*** *****v**g kl*ag***** p*****cl**
Consensus -SERYVFKHP RPPKPDAPRI YEAHVGM SGE EPEVSTYREF ADNVLPRIRA
```

FIG. 4A



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	301				350
RSBEI	*****	*****	*****	*****	*****
MSBEI	*****	*****	*****	*****	*****
D4cDNA	*****	*****ilcf*	w*****	*****	*****
PESBEII	*****	*****	w****kp***	*****s***	*****
POSBE	*****	*****g**	*****	*****y*n**	*****
D2cDNA	t*****g	*****ds***	*****	*****	*****
Consensus	NNYNTVQLMA	IMEHSYYASF	GYHVTN-FFA	VSSRSGTPED	LKYL-DKAHS
	351				400
RSBEI	*****	*****	*****n	*h*****t**	*****
MSBEI	*****	*****	*****	*****a**	*****
D4cDNA	*****	*****s*m**	*****n	*****t**	*****
PESBEII	***n*****	*****	*****	s*q*****a**	*****
POSBE	***q**v***	*****	*****g	s*****a**	*****
D2cDNA	*****	*****i*	*****	ah****yt**	k*n***ng*
Consensus	LGLRVLMDVV	HSHASNNVTD	GLNGYDVGQS	TQESYFH-GD	RGYHKLWDSR
	401				450
RSBEI	*****	*****	*****	*****	*****k****
MSBEI	*****	*****	*****	*****	*****v****
D4cDNA	*****	*****	*****	*****n	*****s*a*
PESBEII	*****ks.	s*****	*****k*****	*****	*****a***
POSBE	*****	*****	*****n*****	*****v	*****
D2cDNA	*****	*****	*****	*v*****n	*n*****s*n*
Consensus	LFNYANWEVL	RFLLSNLRW	-DEFMFDGFR	FDGVTSMLYH	HHGINMGFTG
	451				500
RSBEI	*****	*****	*****l**	*****	*****
MSBEI	**q*****	a*****	*****l**	*****	*****
D4cDNA	*****g***	*****	*****i**	*****	*****s**
PESBEII	d*n****e**	*****	**s*v*di**	***d*****	***g*g***s
POSBE	**n****ea*	*****	**n*i*i**	*****	***g*g***s
D2cDNA	***ig***	n***f*****	*****l**	**i***v***	*****
Consensus	NYKEYFSLDT	DVDAVVYMLL	ANHLMHK-LP	EATVVAEDVS	GMPVLCRPVD
	501				550
RSBEI	*****	*****	*****rk*	****.*vq**	*****
MSBEI	*****	*****	*****	**g*.ah**	*****
D4cDNA	*****	*****	*****l**	***a.*ah**	*****
PESBEII	*v*****	*****k***	*****k****	**k*.sln*	*****
POSBE	*****	*****k***	*****n*e**	**k*.tss*	*****
D2cDNA	***l*****q	**t*****	**e**g*qq*	***sv*sq**	*****p**f*
Consensus	EGGVGFYRL	AMAIPDRWID	YLKNKDDSEW	SMSE-I--TL	TNRRYTEKCI
	551				600
RSBEI	*****	*****	*****t***	*****n	*****
MSBEI	*****	*****	*****t***	*****	*****
D4cDNA	*****	*****m****	*****t***	*****	*****
PESBEII	s*****	*****	**e***ss**	c*tml*****	***s*h****
POSBE	*****	*****	*****s***	c*td***v**	*****h****
D2cDNA	****rqnh**	**s**m****	**w*t*s***	a*d*d*****	*a*****
Consensus	AYAESHQSI	VGDKTIAFL	MDKEMY-GMS	DLQPASPTID	RGIALQKMIH

FIG. 4B



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	601		650
RSBEI	*****	*****	*****
MSBEI	*****	*****	*****
D4cDNA	*****	*****	*****
PESBEII	*****	*****	*****
POSBE	*f*****	*****	*****
D2cDNA	*****s	**k*****	*****
Consensus	FITMALGGDG	YLNFMGNEFG	HPEWIDFPRE GNNWSYDKCR -RQWSLVDTD
	651		700
RSBEI	*****	*****e	*****k***
MSBEI	*****	*****r	*****
D4cDNA	*****	*****	*****k***
PESBEII	*****	*r***l***	**i*a*t***
POSBE	*****	*r***s***	*****a*g***
D2cDNA*****	v**vdtps**	c*****nt a*h*****g
Consensus	HLRYKYMNAF	DQAMNALD-K	FSFLSSSKQI VSDMNEE-KV IVFERGDLVF
	701		750
RSBEI	*****n***	k*****	*****
MSBEI	*****k***	*****	*****
D4cDNA	*****s***	*****	*****
PESBEII	*****en**	*****	*****
POSBE	*****kn**	*****	*****
D2cDNA	.*thlrsgc*	*p.....s**	stssc**... *
Consensus	VFNFHP-KTY	EGYKVGCDLP	GKYRVALDSD AL-FGGHGRV GHDVDHFTSP
	751		800
RSBEI	**m*****	*****	*****
MSBEI	*****	*****	*****
D4cDNA	*****	*****	*****
PESBEII	*****	*****	*****
POSBE	*****	*****	*****
D2cDNA	ifcc*lfkge	*.....	*****
Consensus	EG-PGVPETN	FNNRP-----	-----NSFKV LSPPRTCVAY
	801		850
RSBEI	*...****dr	**l*rg**va	s**i.vte**
MSBEI	*...****ag	agr*lhak*e	t***s**es*
D4cDNA	*...****ka	*kpkde****	w**aa*g.**
PESBEII	*...****q	**snnpnlg*	*ee**a*adt
POSBE	*yqqp*sr*v	trnlkirylq	*sv**tna*q
D2cDNA
Consensus	Y---RVDER-	EE-R--GAAS	-GKT-PA-YI DV-ATR---- -SGE--SG--
	851		876
RSBEI	kg***d*cg*	**mk***r**	*e*c*d
MSBEI	edk*atagg*	**wk*arqp*	*q*t**
D4cDNA	ka*tg*ss*	**in***g*p	*k*n*.
PESBEII	r*e*ns**av	dagi*kvere	vvgdn*
POSBE	r*tr*lk*sl	stnist*...
D2cDNA
Consensus	--SEK-DD-K	KG--FVF-SS	D-D-K-

FIG. 4C



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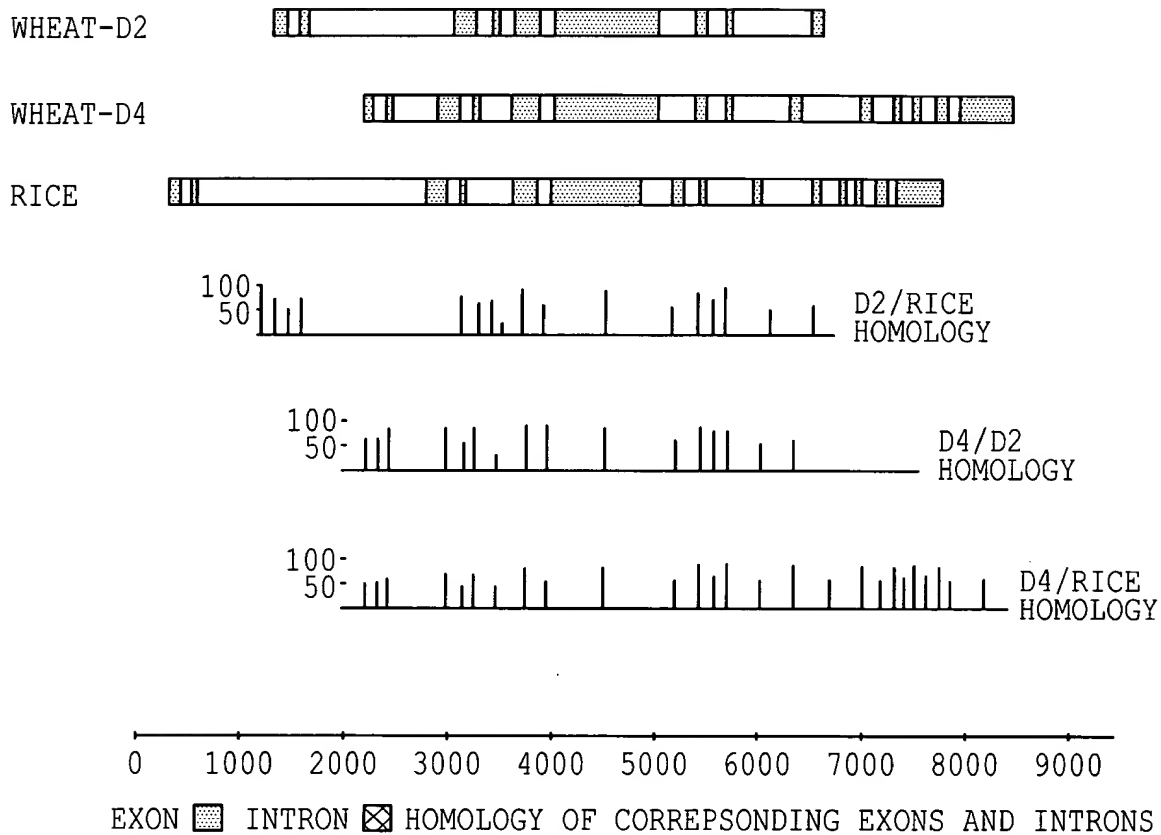


FIG. 5



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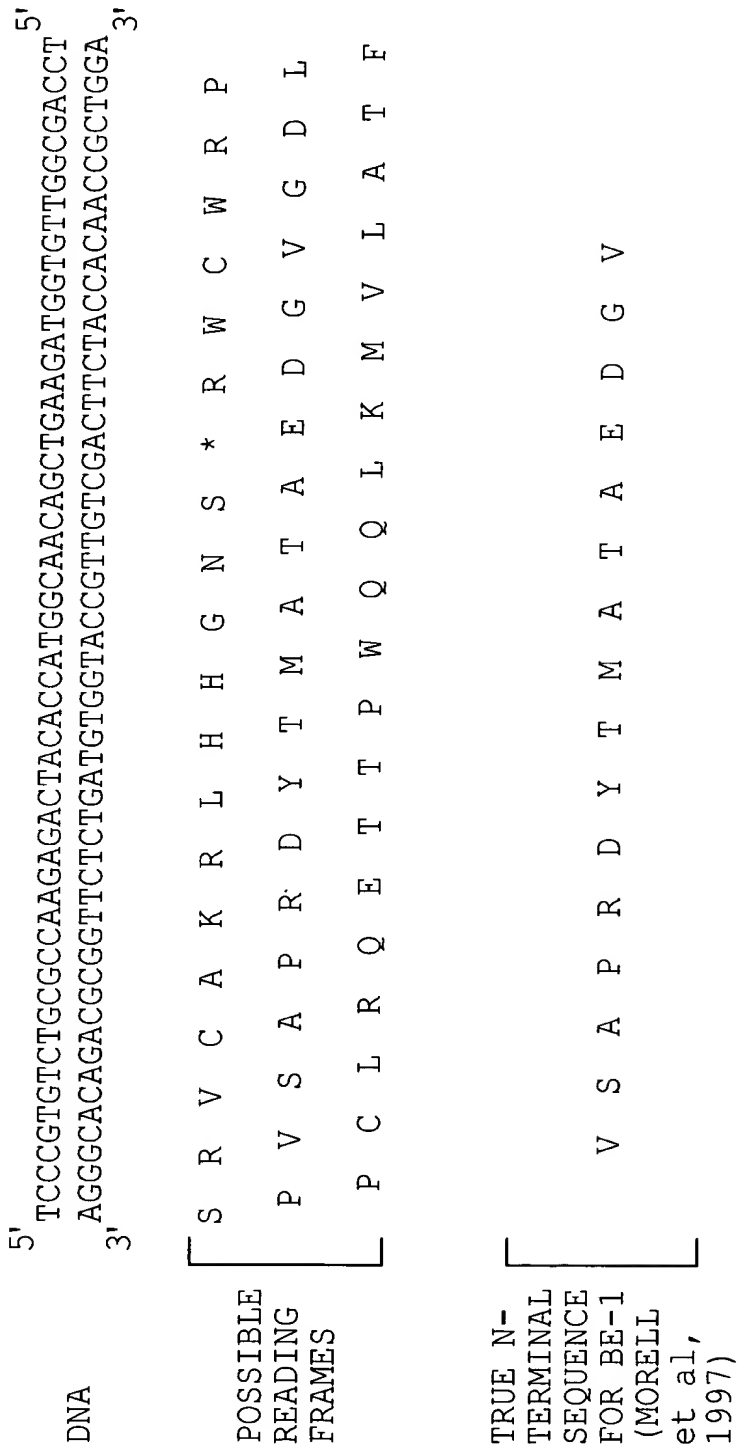


FIG. 6



FIG. 7A

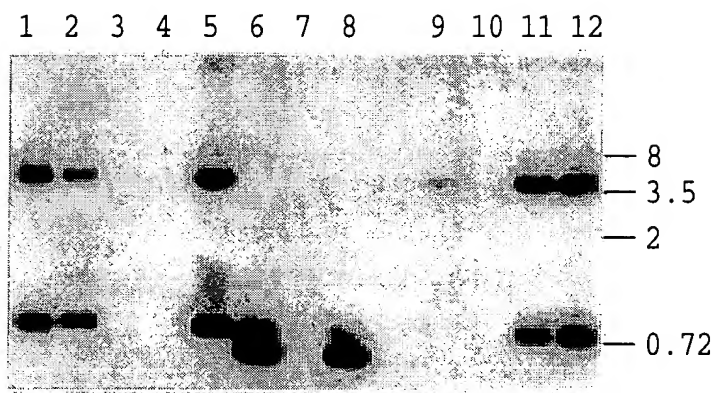
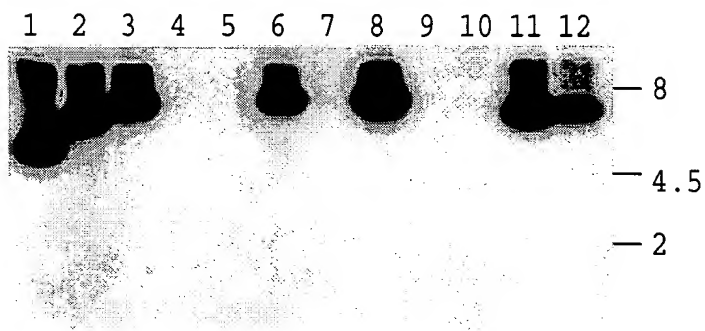


FIG. 7B



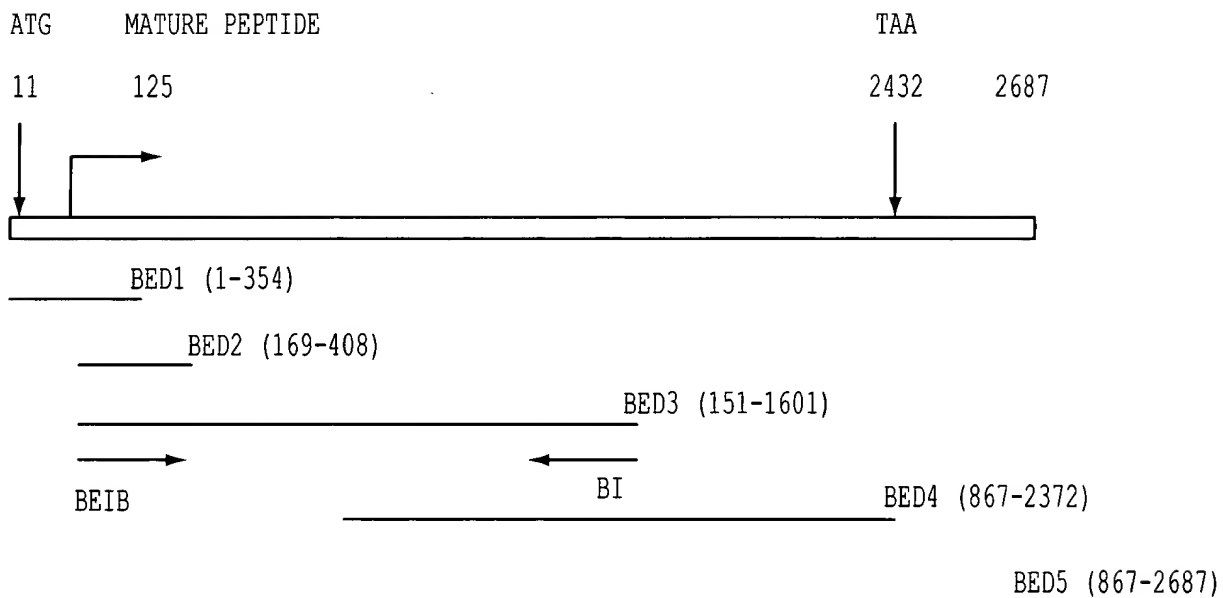


FIG. 8



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EXPRESSION OF STARCH BIOSYNTHETIC GENES

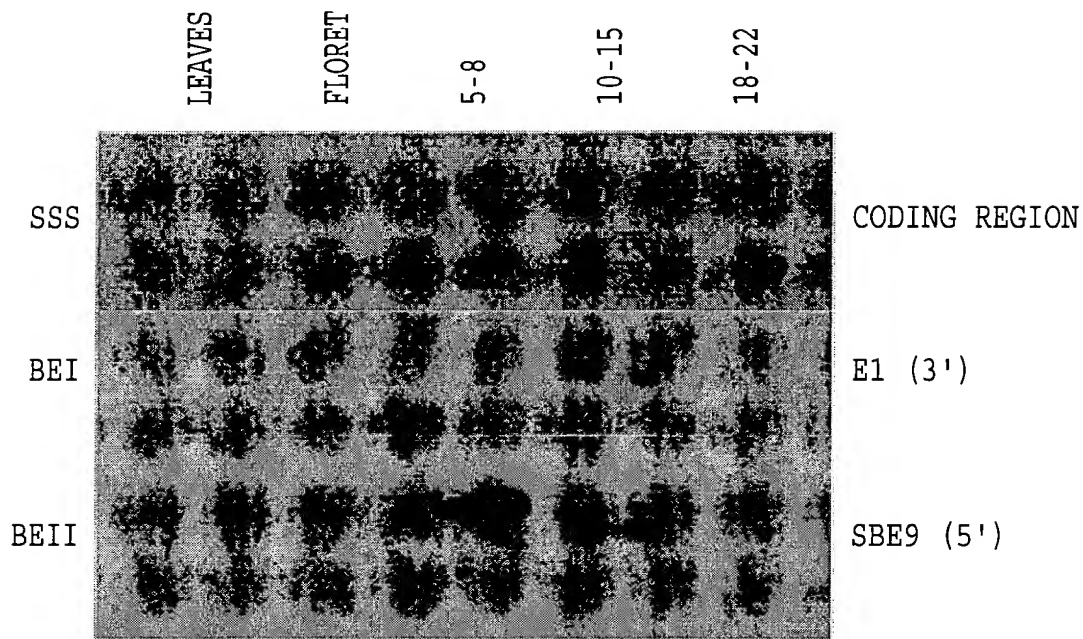


FIG. 9A



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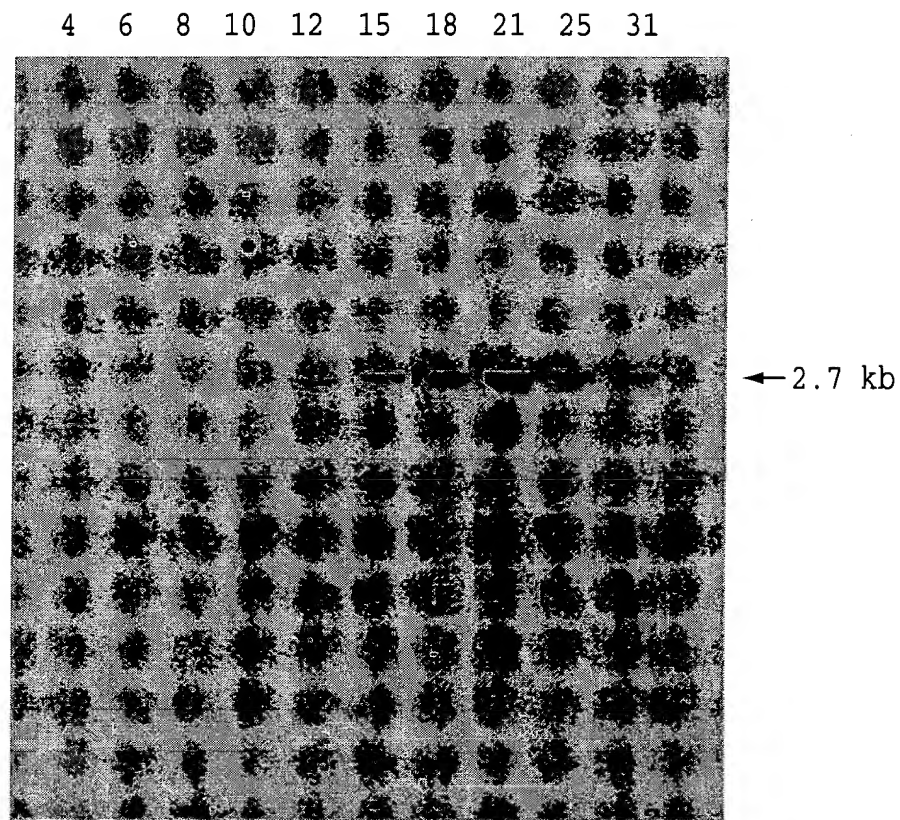


FIG. 9B



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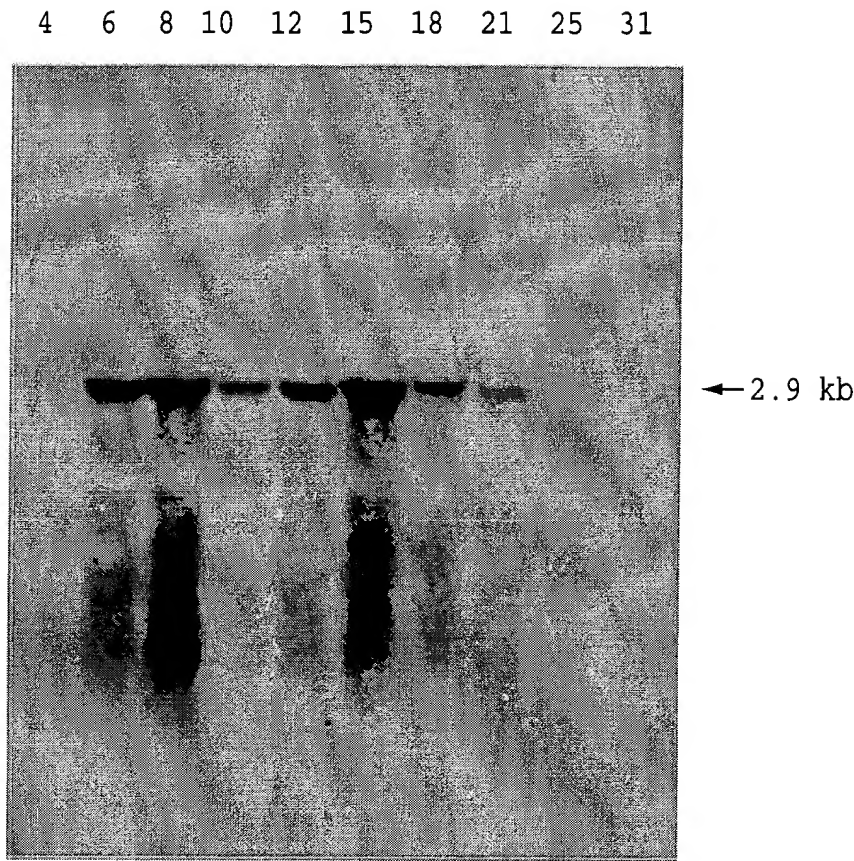


FIG. 9C



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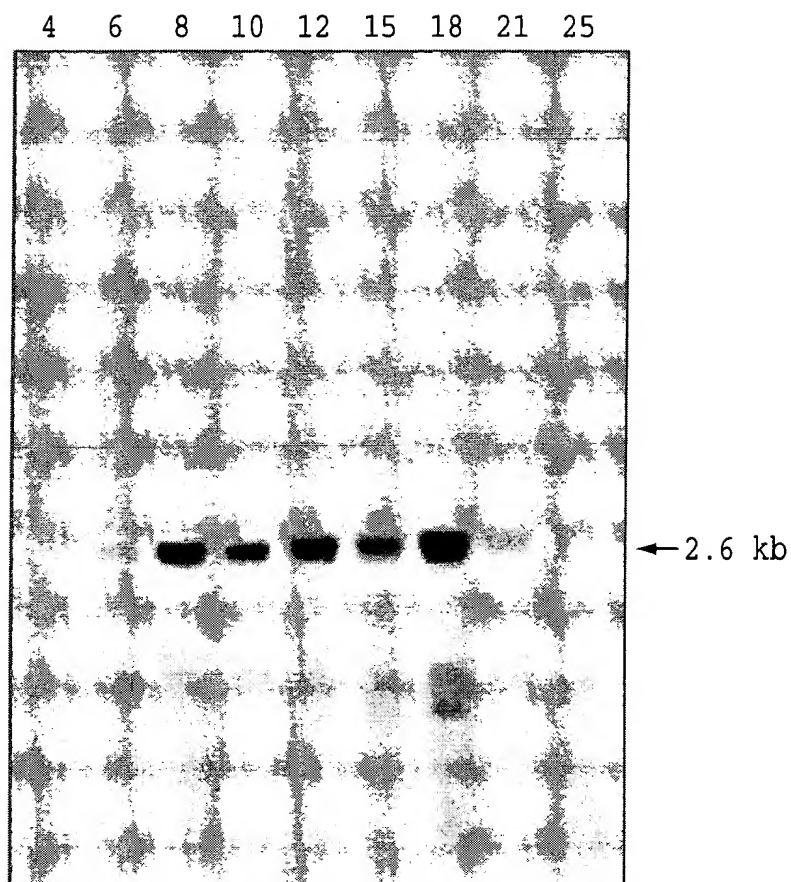


FIG. 9D



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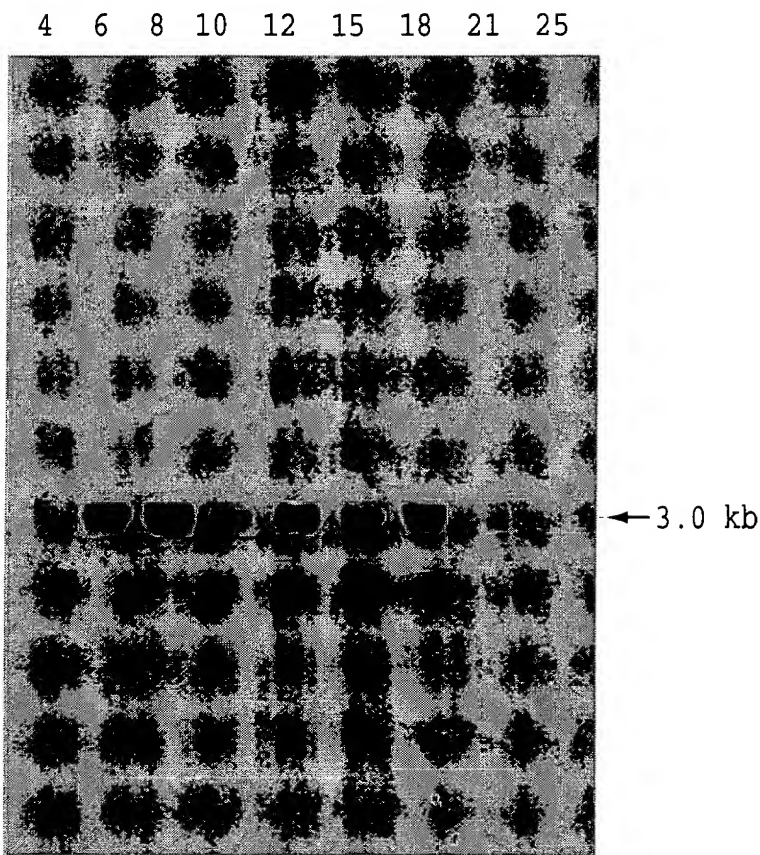


FIG. 9E



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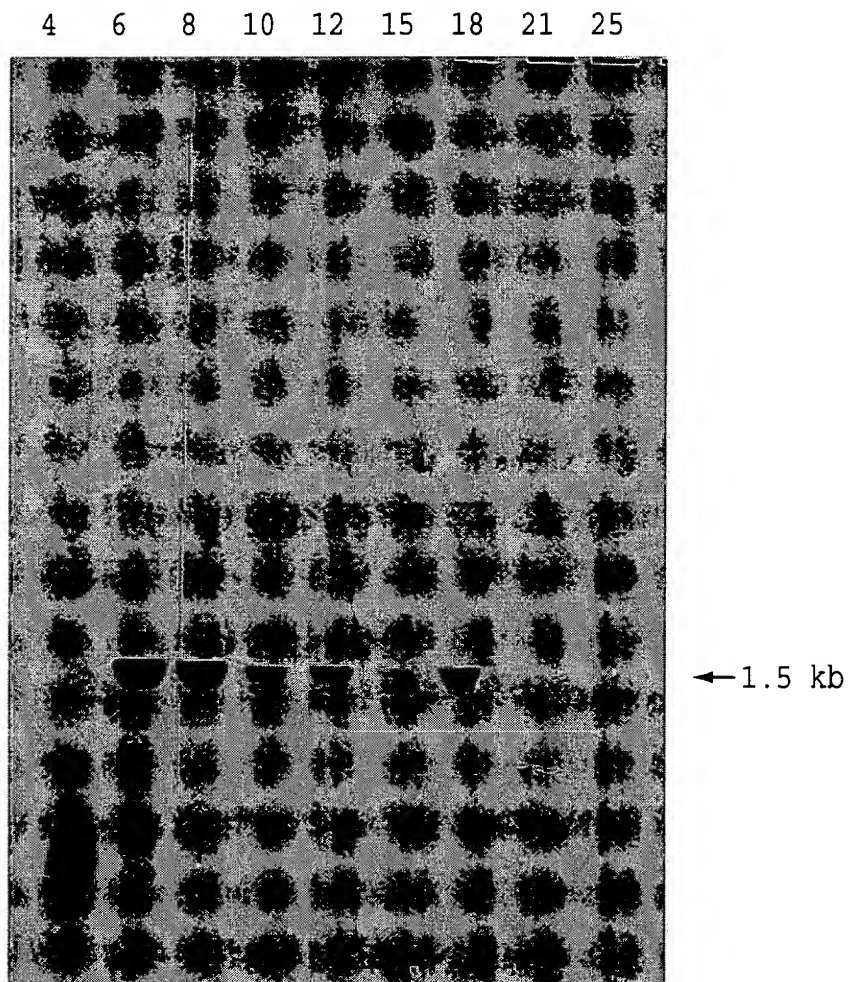


FIG. 9F



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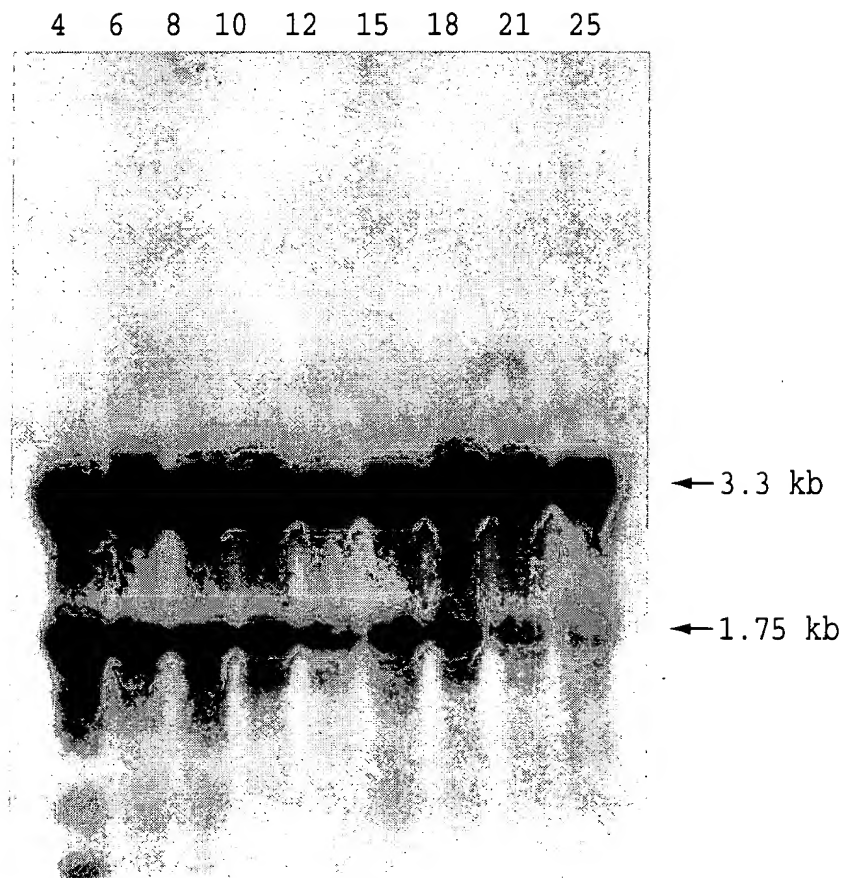


FIG. 9G



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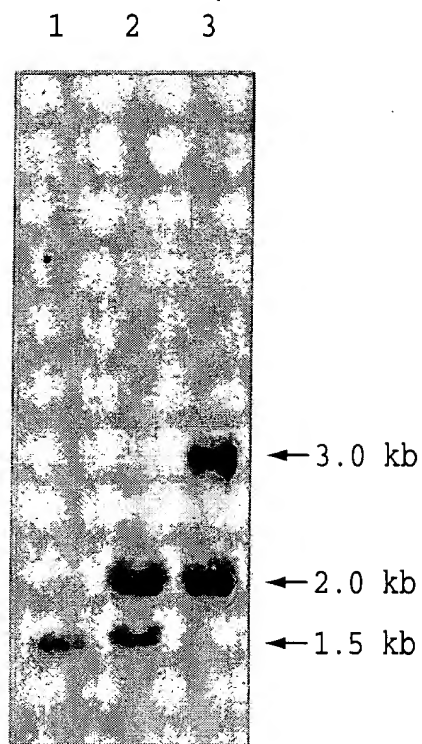


FIG. 9H



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COMPARE WINDOW: 21 STRINGENCY: 14.0 POINTS: 20,788

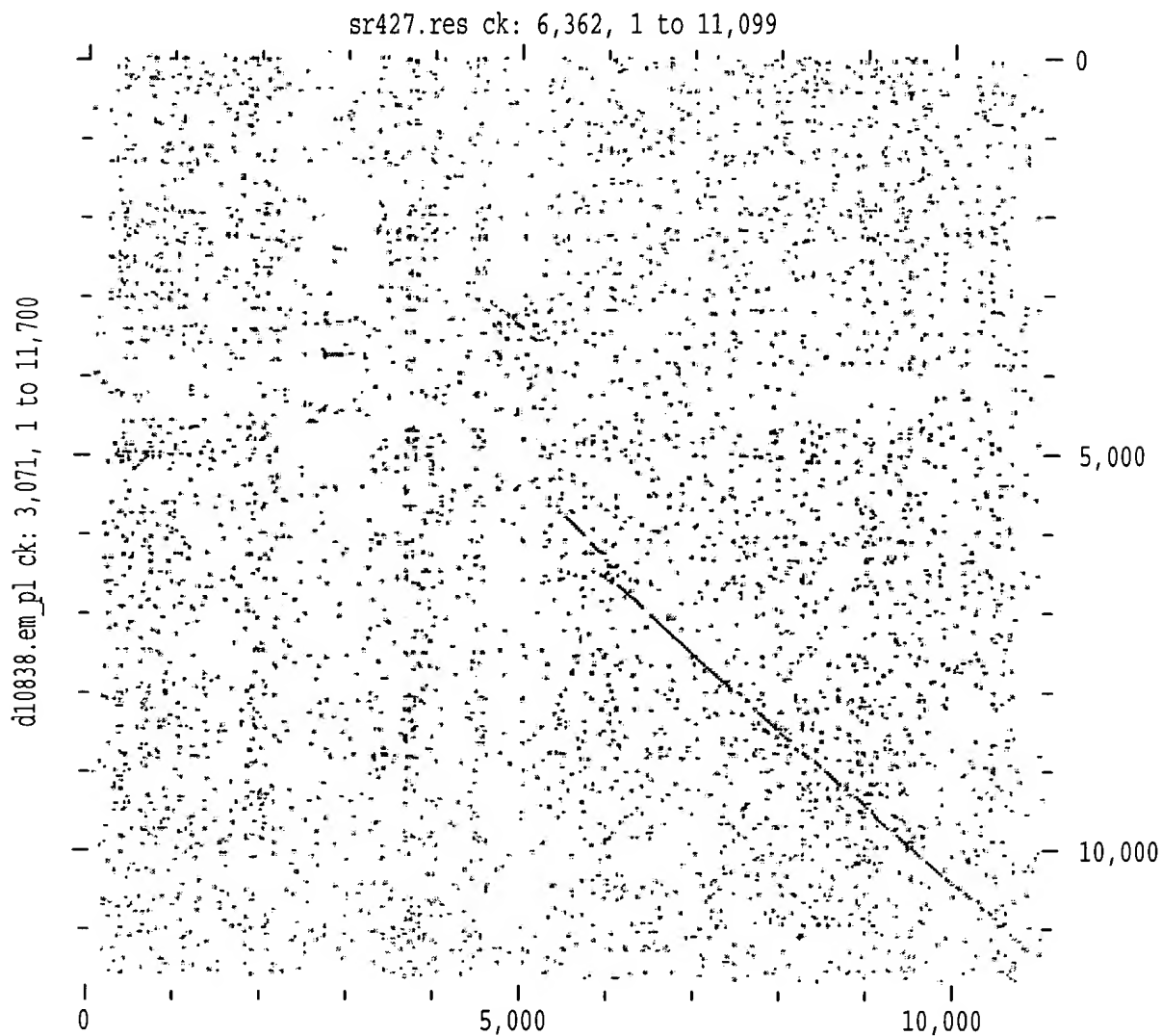
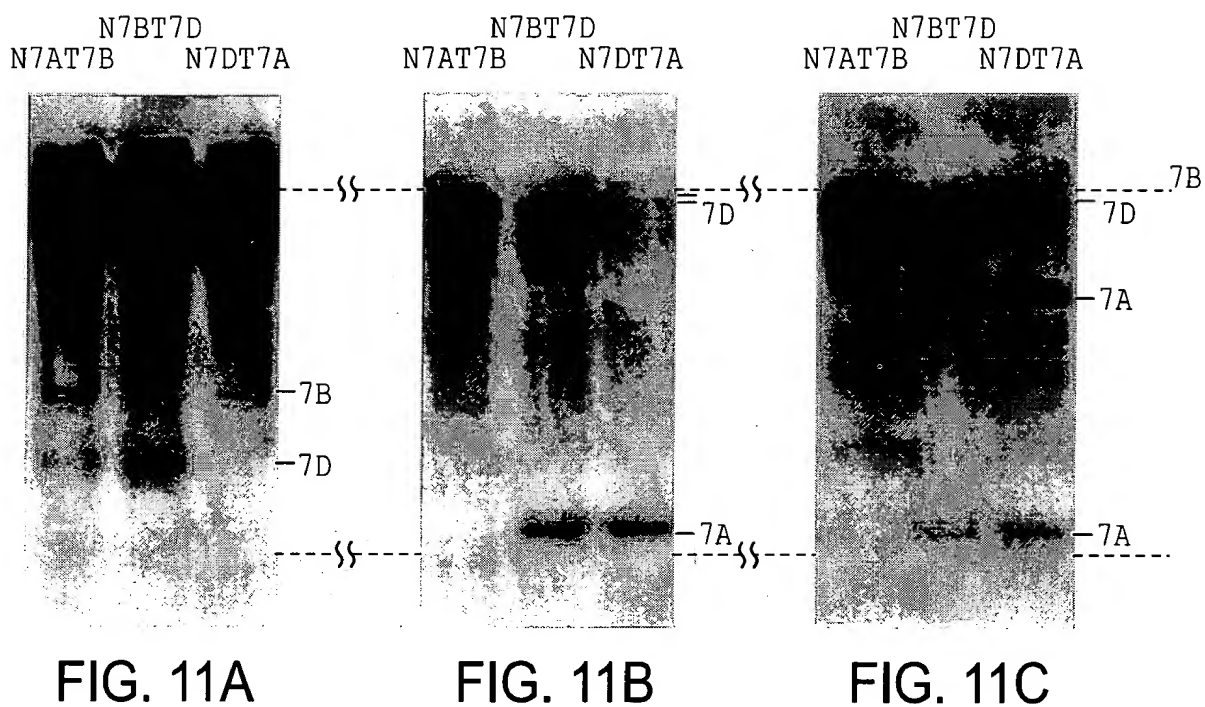


FIG. 10





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GENOMIC CLONES FROM *T. tauschii*
FOR SBE II.

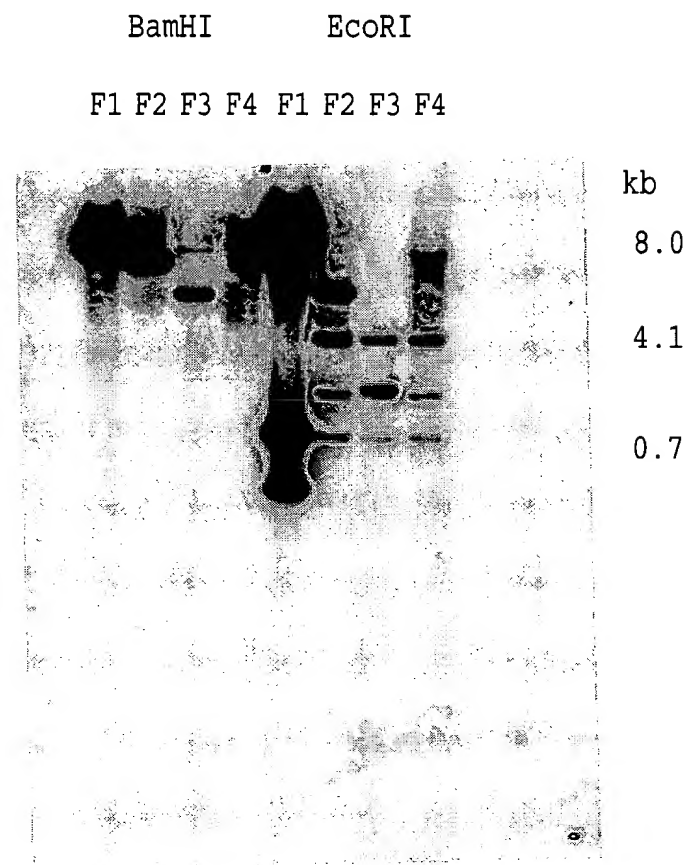


FIG. 12



N-TERMINAL SEQUENCES OF CEREAL STARCH BRANCHING ENZYMES

PROTEIN	1	2	3	4	5	6	7	8	9	1	1	1	1	1	1	1	1	1	2	2	2	
	A									0	1	2	3	4	5	6	7	8	9	0	1	2
RICEBEI ^B	A	T	A	R	K	N	K	T	M	V	T	V	V	E	E	V						
WBE-I ^{AD}	V	S	A	P	R	D	Y	T	M	A	T	A	E	D	G	V						
MAIZE	A	T	V	Q	E	D	K	T	M	A	T	A	K	G	D	V						
BEI ^C																						
RICEBEII ^D	A	A	G	A	S	G	E	-	V	M	I	P	E	G	E	S	D	G	M	P	V	S
WBE-II		A	A	S	P	G	K	-	V	L	V	P	D	G	E	S	D	D	L	A	S	Y
MAIZE	A	A	A	A	A	R	K	A	V	M	V	P	E	G	E	N	D	G	L	A	S	
BEII ^B																						

A N-TERMINAL AMINO ACID OF THE MATURE POLYPEPTIDE.
 B KAWASAKI *et al.* (1993),
 C BABA *et al.* (1991),
 D MIZUNO *et al.* (1993),
 E FISHER *et al.* (1993)

RESIDUES IN THE WHEAT SEQUENCES SHOWING IDENTITY WITH THE RESPECTIVE MAIZE OR RICE BRANCHING ENZYME ISOFORMS ARE HIGHLIGHTED IN BOLD TEXT.

FIG. 13A



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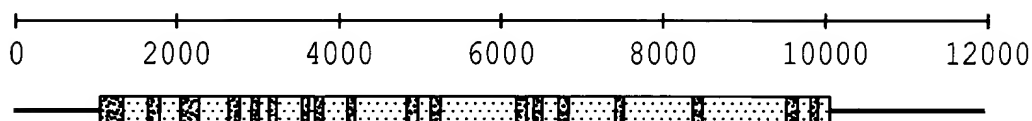
TTCCCTTTTTTTTTCTTTGGGNGGGGGATGGCCTGTTGGATGNTGTTCCCCAATGAATTT
1 -----+-----+-----+-----+-----+ 60
AAGGGAAAAAAGAAACCCNCCCCCTACCGGACAACCTACNACAAGGGGTTACTTAA
a F P F F F F G ? G M A C W M ? F P N E F -
b S L F F S L G G G W P V G ? C S P M N F -
c P F F F L W ? G D G L L D ? V P Q * I S -
CCATGGAGTGAGAGAGATAGTTGGATNAGGGATCGCGNTTCNGGAAGTGTATTTTTTTC
61 -----+-----+-----+-----+-----+ 120
GGTACCTCACTCTCTCTATCAACCTANTCCCTAGCGCNAAGGNCCTTGACATAAAAAAAG
a P W S E R D S W ? R D R ? S ? N C I F F -
b H G V R E I V G ? G I A ? P G T V F F S -
c M E * E R * L D ? G S R F ? E L Y F F P -
CCCNGCGGGGGAAATGGCGTTAGTGTACCCAGGCCCTGGTGTACCACGGCTTTGATC
121 -----+-----+-----+-----+-----+ 180
GGGNCGCCCCCTTTACCGCAATCACAGNTGGGTCCGGGACCACAATGGTGCCGAAACTAG
a P ? G G N G V S V ? P G P G V T T A L I -
b P A G E M A L V S T Q A L V L P R L * S -
c ? R G K W R * C ? P R P W C Y H G F D H -
ATTCTTCGTTTCATTCTGATATATATTTTCTCATTCTTTTCTTCCTGTTCTTGCTGTAA
181 -----+-----+-----+-----+-----+ 240
TAAGAAGCAAAGTAAGACTATATATAAAAGAGTAAGAAAAAGAAGGACAAGAACGACATT
a I L R F I L I Y I F S F F F F L F L L * -
b F F V S F * Y I F S H S F S S C S C C N -
c S S F H S D I Y F L I L F L P V L A V T -
CTGCAAGTTGTGGCGTTTTTTCATTATTGTAGTCATCCTTGCAATTTTGCAGGCGCGTCC
241 -----+-----+-----+-----+-----+ 300
GACGTTCAACACCGCAAAAAAGTGATAACATCAGTAGGAACGTAAAACGTCCGCGGCAGG
a L Q V V A F F H Y C S H P C I L Q A P S -
b C K L W R F F T I V V I L A F C R R R P -
c A S C G V F S L L * S S L H F A G A V L -
TGAGCCGCGCGGCTCTCCAGGGAAGGTCCTGGTGCCTGACGGCGAGAGNACGACTTGG
301 -----+-----+-----+-----+-----+ 360
ACTCGGCGCGCGGAGAGGTCCCTTCCAGGACCACGGACTGCCGCTCTCNCTGCTGAACC
a * A A R P L Q G R S W C L T A R ? T T W -
b E P R G L S R E G P G A * R R E ? R L G -
c S R A A S P G K V L V P D G E ? D D L A -
CAAGTCCGGCGCAACCTGAAGAATTACAGGTACACACACTCGTGCCGGTAAATCTTCATA
361 -----+-----+-----+-----+-----+ 420
GTTCAGGCCGCGTTGGACTTCTTAATGTCCATGTGTGTGAGCACGGCCATTTAGAAGTAT
a Q V R R N L K N Y R Y T H S C R * I F I -
b K S G A T * R I T G T H T R A G K S S Y -
c S P A Q P E E L Q V H T L V P V N L H T -
CAATCGTTATTCACTTACCAAATGCCGGATGAAACCAACCACGGATGCGTCAGGTTTCGA
421 -----+-----+-----+-----+-----+ 480
GTTAGCAATAAGTGAATGGTTTACGGCCTACTTTGGTTGGTGCCTACGCAGTCCAAAGCT
a Q S L F T Y Q M P D E T N H G C V R F R -
b N R Y S L T K C R M K P T T D A S G F E -

FIG. 13B



BRANCHING ENZYME-II GENES

INTRON/EXON STRUCTURE OF WHEAT BE-II



SCHEMATIC DIAGRAM OF A cDNA BE-II

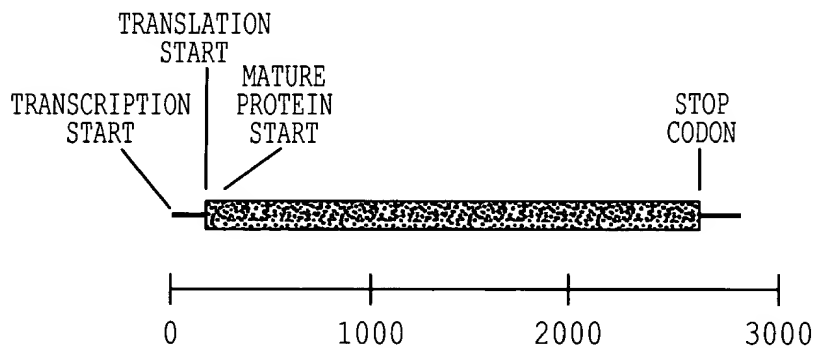


FIG. 14



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WHEAT DNA PROBED WITH THE
5' CONSERVED SEQUENCE OF SBE II.

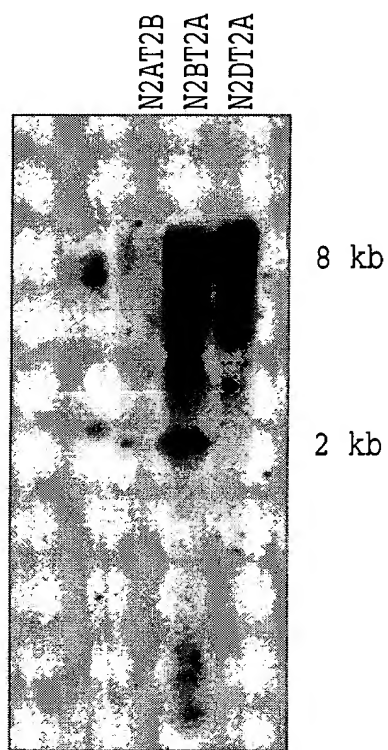


FIG. 15



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COMPARISON OF N-TERMINAL SEQUENCES
OF SOLUBLE STARCH SYNTHASE

GRYVAELSREGPAARP	DEDUCED FROM WHEAT cDNA
GPYVAELSPGPAAPP	WHEAT N-TERMINAL

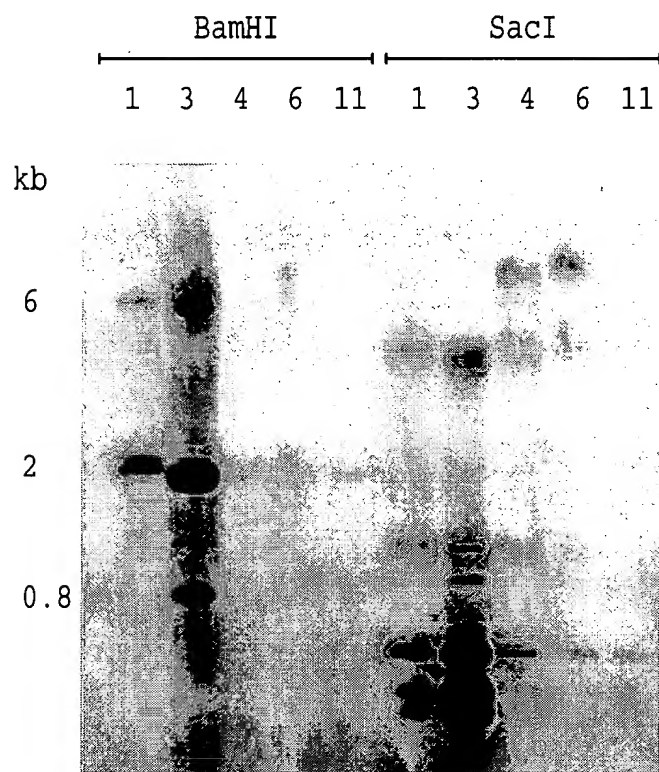
FIG. 16



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SOLUBLE STARCH SYNTHASE GENOMIC CLONES



PROBED WITH SM-2 FULL LENGTH cDNA

FIG. 17

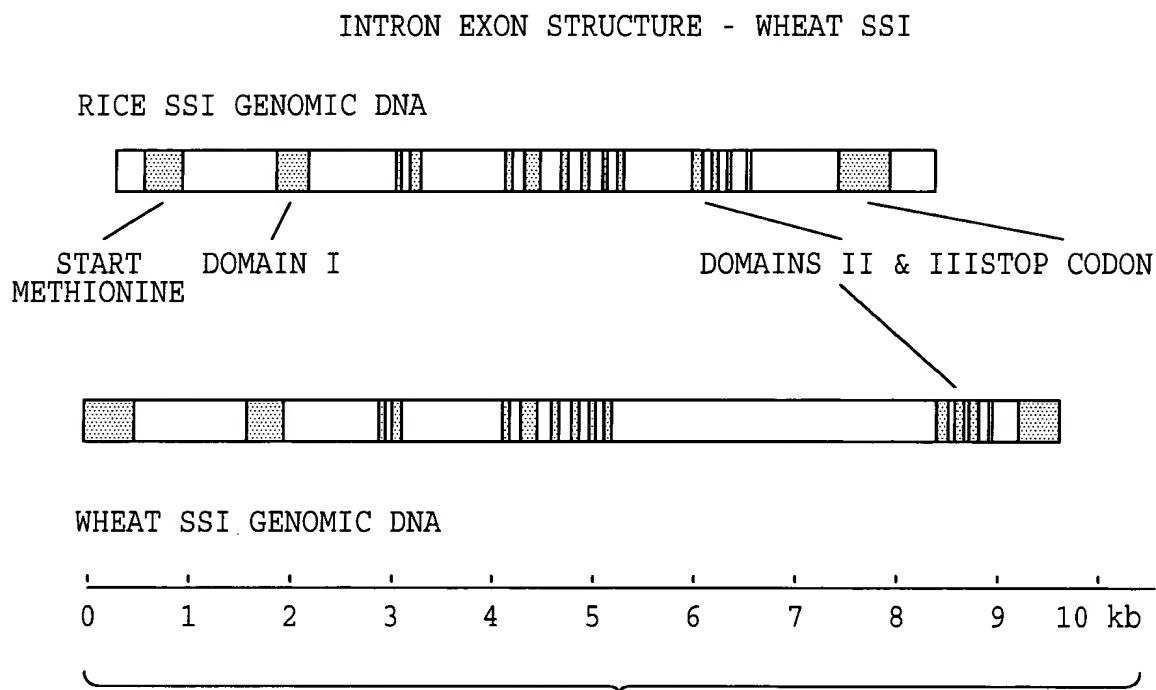


FIG. 18



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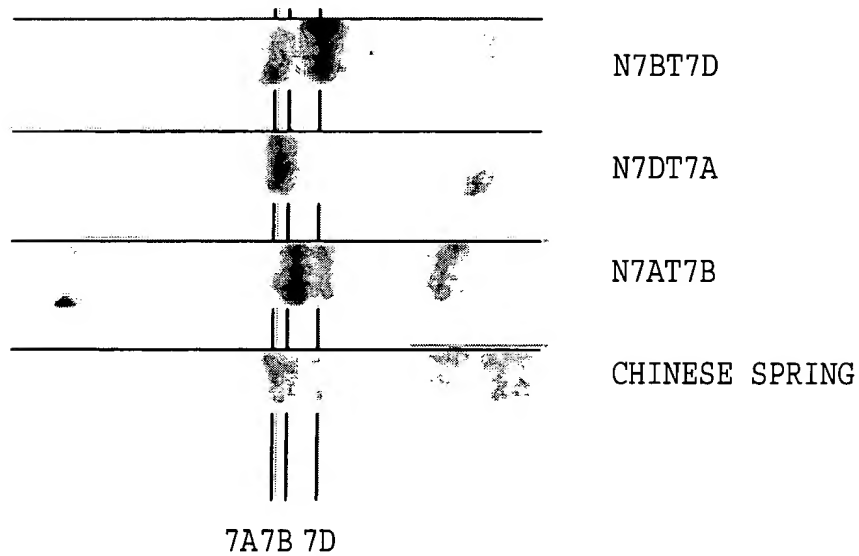


FIG. 19



```
      ATACTACATACTATATGCTTGCACCCAAGGGACACTTTTATAACTATTCTGGCTGTGGGA
80  +-----+-----+-----+-----+-----+-----+-----+-----+ 139
      TATGATGTATGATATACGAACGTGGGTTCCCTGTGAAAATATTGATAAGACCGACACCCT

a      T T Y Y M L A P K G H F Y N Y S G C G N -
b      I L H T I C L H P R D T F I T I L A V G -
c      Y Y I L Y A C T Q G T L L * L F W L W E -

      ATACCTTCAACTGTAATCATCCTGTGGTTCGTCAATTCATTGTAGATTGTTTAAGATACT
140 +-----+-----+-----+-----+-----+-----+-----+-----+ 199
      TATGGAAGTTGACATTAGTAGGACACCAAGCAGTTAAGTAACATCTAACAAATTCTATGA

a      T F N C N H P V V R Q F I V D C L R Y W -
b      I P S T V I I L W F V N S L * I V * D T -
c      Y L Q L * S S C G S S I H C R L F K I L -

      GGGTGACGGAAATGCATGTTGATGGTTTTTCGTTTTGACCTT
200 +-----+-----+-----+-----+-----+-----+ 240
      CCCACTGCCTTTACGTACAAC TACCAAAAGCAAAACTGGAA

a      V T E M H V D G F R F D L -
b      G * R K C M L M V F V L T -
c      G D G N A C * W F S F * P -
```

ENZYMES THAT DO CUT:

NONE

ENZYMES THAT DO NOT CUT:

EcoRI

FIG. 20A



COMPARISON OF WHEAT DEBRANCHING ENZYME-I (WDBE-I) PCR FRAGMENT WITH
MAIZE SUGARY-1 DNA SEQUENCE

```

SUGARY.DNA      1098      1107      1117      1127      1137      1147      1157
                TGAGGTGATCATGGATGTTGTCTTCAATCATAACAGCTGAAGGTAATGAGAAAGGCCCAAT
                |||
WHEAT1.DNA      ....GTGATCATGGATGTTGTCTTCAACCATAACAGCTGAGGGTAATGAGAATGGTCCAAT
                -3         6         16        26        36        46        56

FILE NAME      1158      1167      1177      1187      1197      1207      1217
SUGARY.DNA      ATTATCCTTTAGGGGGATAGATAATAGTACATACTACATGCTTGACCTAAGGGAGAGTT
                |||
WHEAT1.DNA      ATTATCATTAGGGGGGTCGATAATACTACATACTATATGCTTGACCCCAAGGGACACTT
                57        66        76        86        96       106       116

FILE NAME      1218      1227      1237      1247      1257      1267      1277
SUGARY.DNA      TTATAATTATTCTGGTTGTGGAAATACCTTCAATTGTAATCATCTGTAGTCCGTGAATT
                |||
WHEAT1.DNA      TTATAACTATTCTGGCTGTGGGNATACCTTCAACTGTAATCATCTGTGGTTCGTCAATT
                117       126       136       146       156       166       176

FILE NAME      1278      1287      1297      1307      1317      1327      1337
SUGARY.DNA      TATAGTGGATTGCTTGAGATACTGGGTAACAGAAATGCATGTTGATGGTTTTTCGTTTTGA
                |||
WHEAT1.DNA      CATTGTAGATTGTTTAAGNTACTGGGTGACGGAATGCATGTTGNTGGTTTTTCGTTTTGA
                177       186       196       206       216       226       236

FILE NAME      1338      1347      1357
SUGARY.DNA      CCTTGCATCTATACT-G...
                |||
WHEAT1.DNA      CCTTGCATCTN--CTTNAAA
                237       246       256
```

MATCHING PERCENTAGE

```

TOTAL WINDOW      84%      (219/260)
ALIGNMENT WINDOW   86%      (219/253)
```

FIG. 20B



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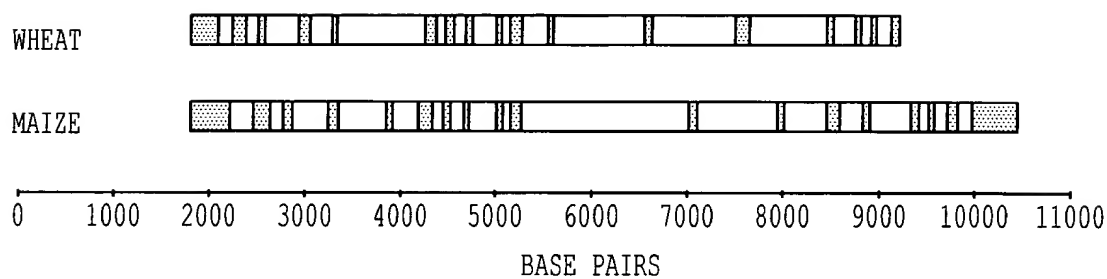


FIG. 20C

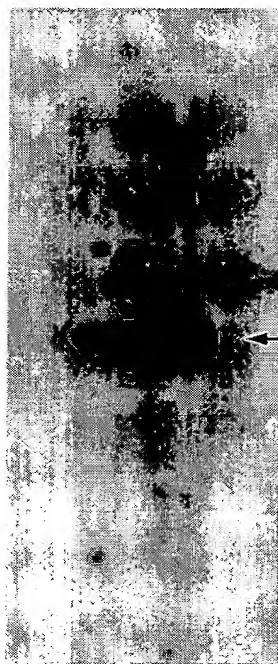


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SOUTHERN BLOT OF *T. tauschii*
GENOMIC DNA

1X 3X



BamHI DIGEST

T. tauschii GENOMIC DNA PROBED
WITH THE WHEAT DEBRANCHING ENZYME
PCR PRODUCT

FIG. 21A

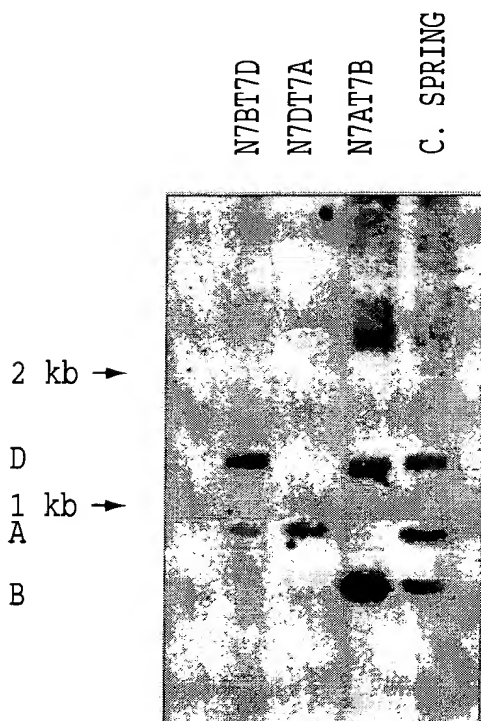


FIG. 21B-1

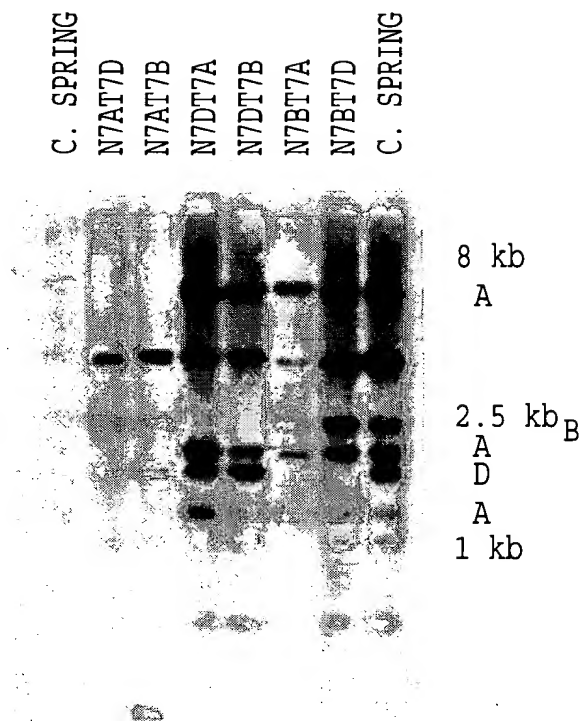


FIG. 21B-2

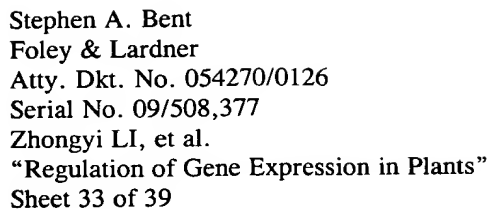


FIG. 22A

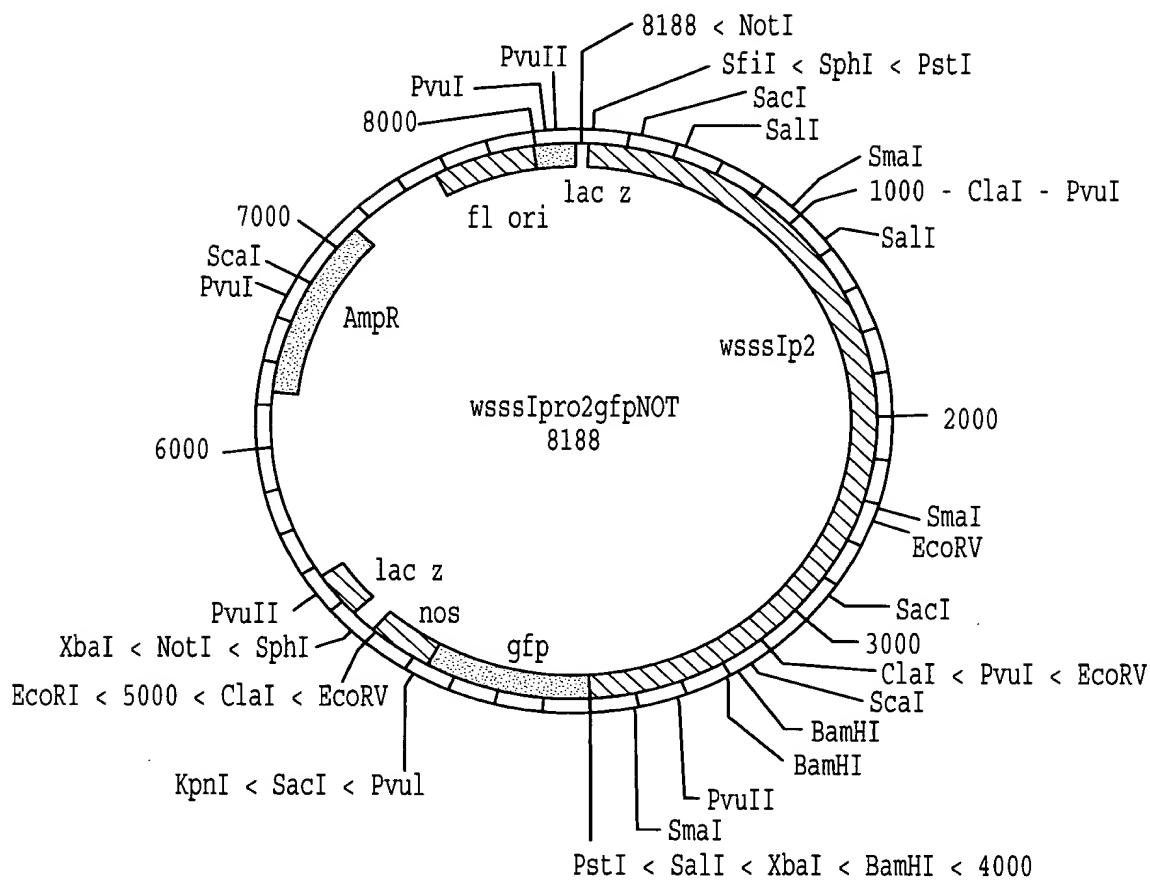


FIG. 22B



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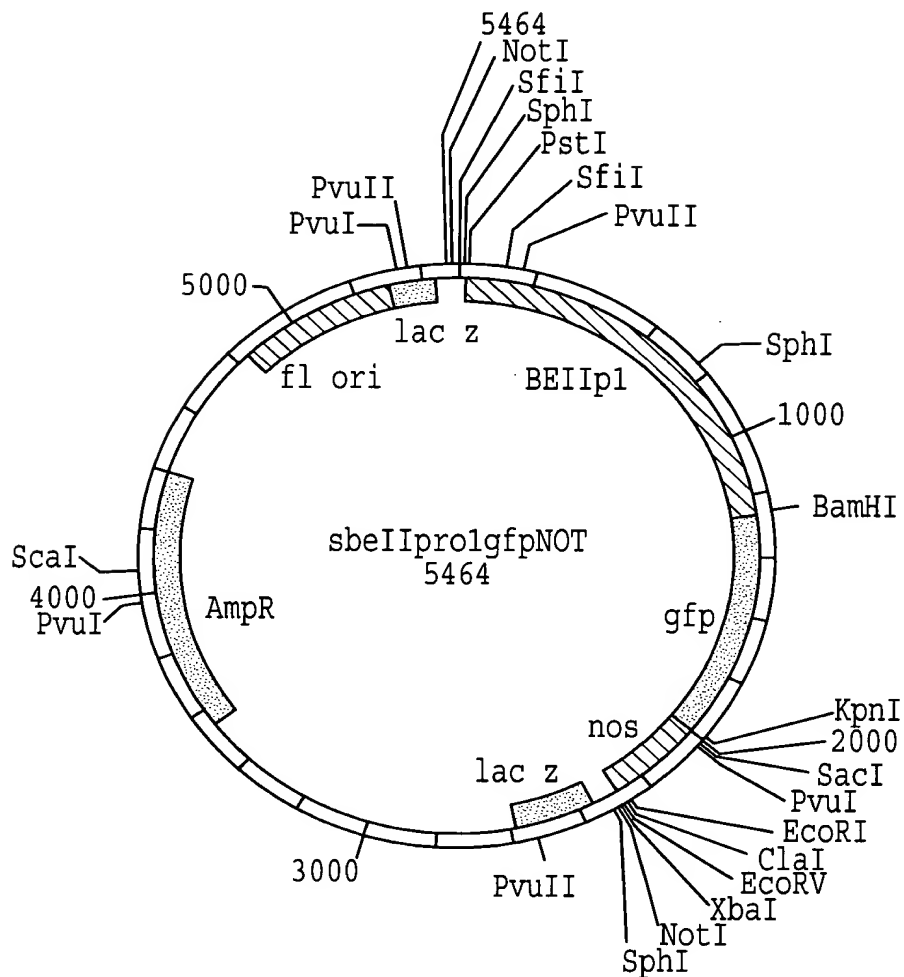


FIG. 22C

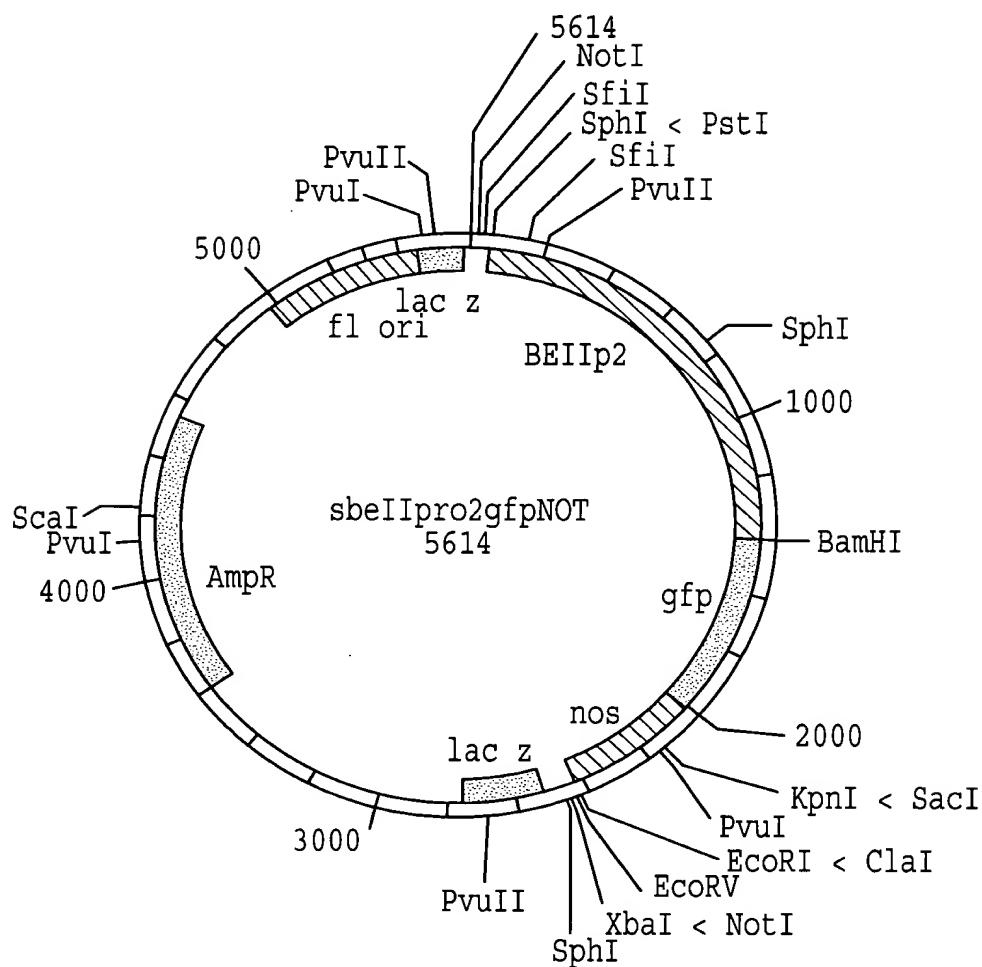


FIG. 22D



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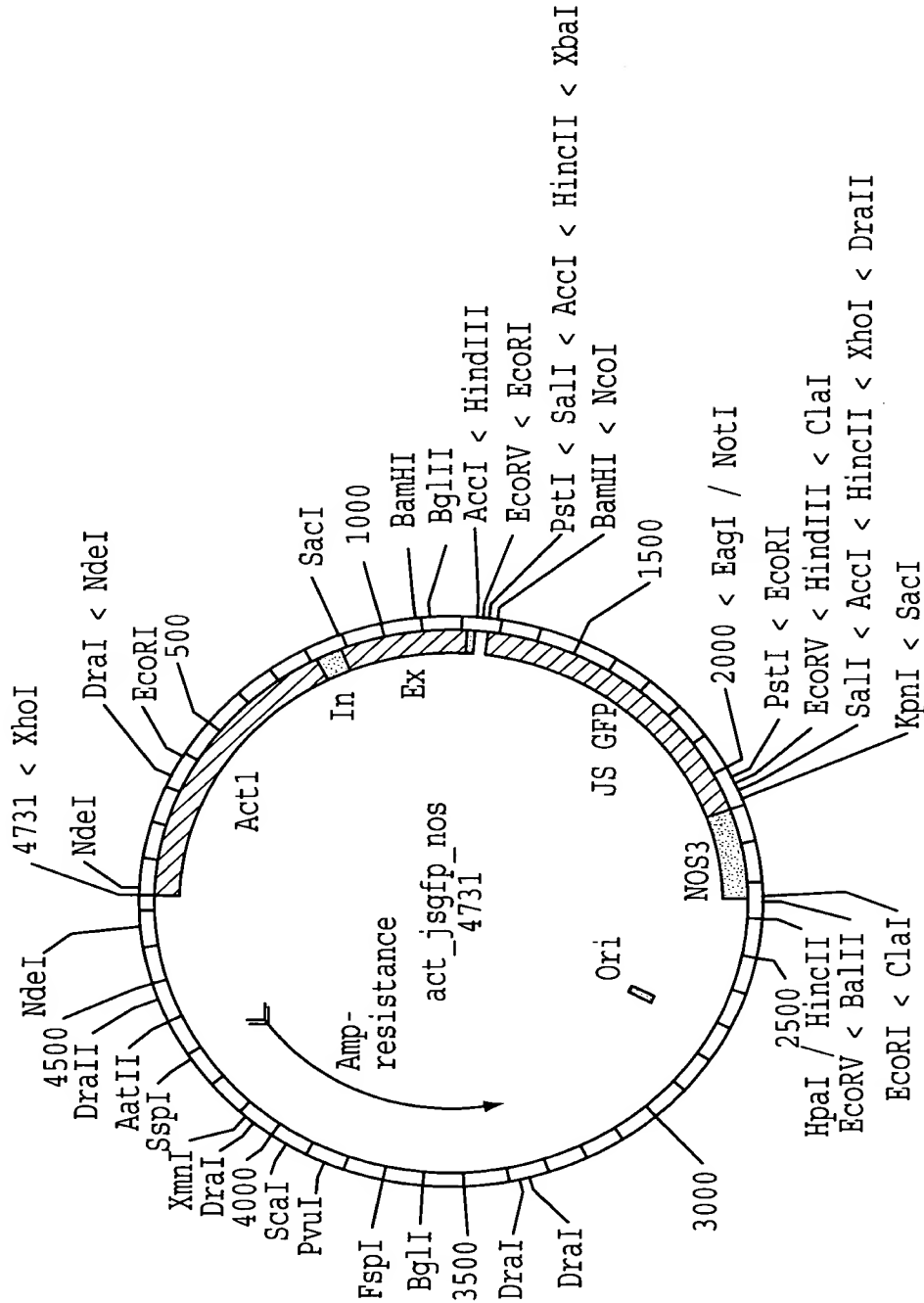


FIG. 22E

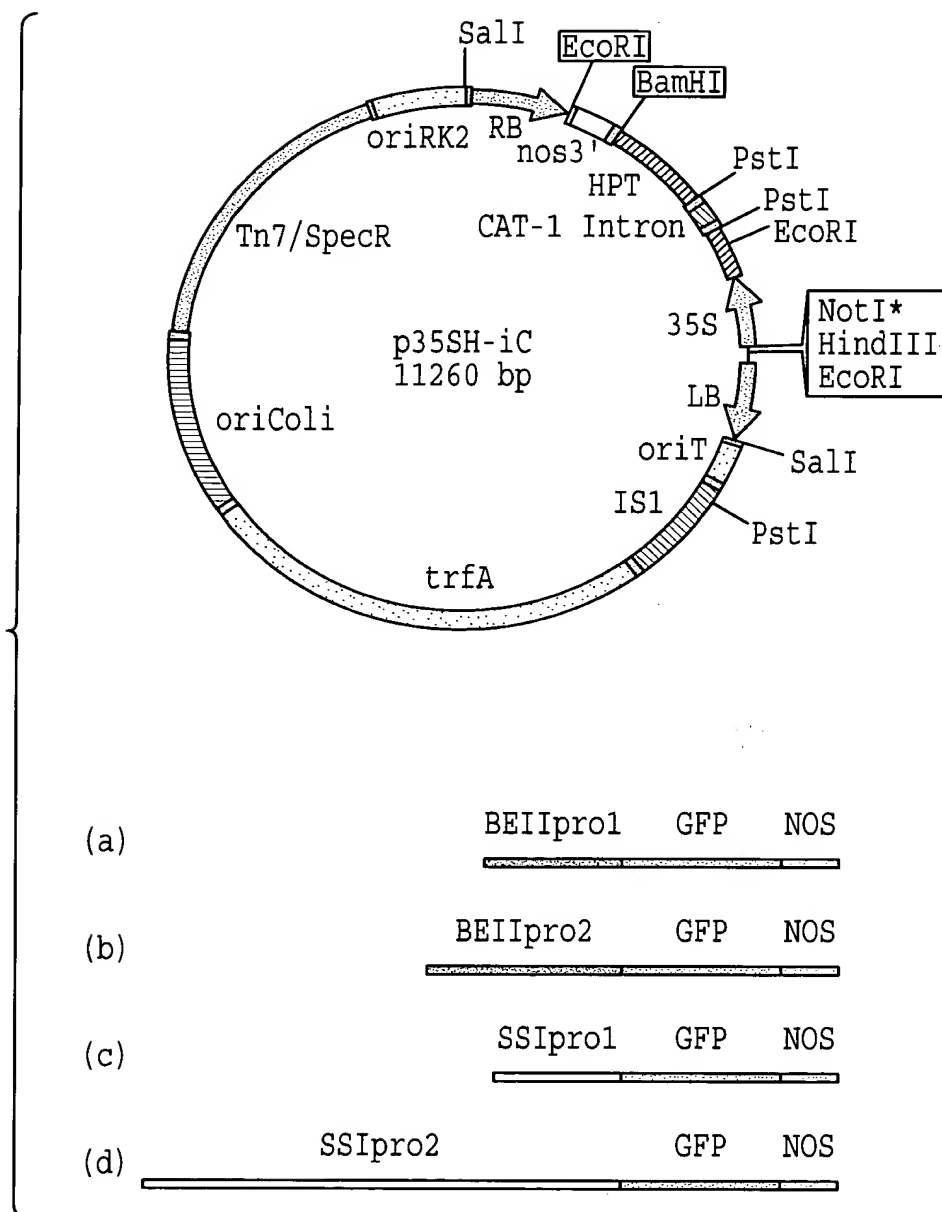


FIG. 23



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FIG. 27A



FIG. 27G



FIG. 27M

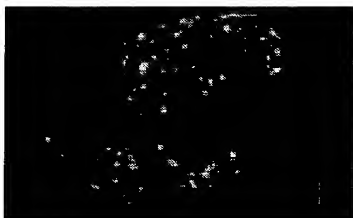


FIG. 27B

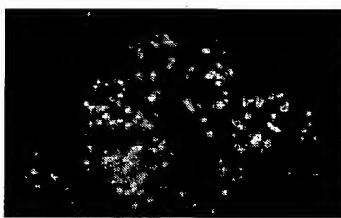


FIG. 27H



FIG. 27N



FIG. 27C

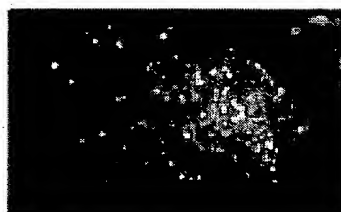


FIG. 27I



FIG. 27O

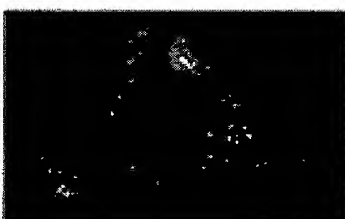


FIG. 27D



FIG. 27J



FIG. 27P

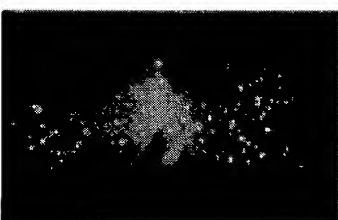


FIG. 27E



FIG. 27K



FIG. 27Q

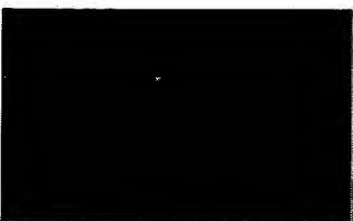


FIG. 27F



FIG. 27L



FIG. 27R